

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David White et al.
Serial No.: 09/195,896
Filed : November 19, 1998
Title : LEPTIN INDUCED GENES

Art Unit:
Examiner:

Box Sequence
Assistant Commissioner for Patents
Washington, DC 20231

VERIFIED STATEMENT UNDER 37 CFR § 1.821 (f)

I, Maureen Ruttle, declare that I personally prepared the paper and the computer-readable copies of the Sequence Listing filed herewith in the above-entitled case and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: Nov 15, 1999

Maureen Ruttle
Maureen Ruttle

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804

Telephone: 617/542-5070
Facsimile: 617/542-8906

Date of Deposit November 29, 1999
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Carrie A. Amonte

SEQUENCE LISTING

<110> White, David
Zhou, Jianghong
Tartaglia, Louis A.

<120> LEPTIN INDUCED GENES

<130> 07334/109001

<140> US 09/195,896

<141> 1998-11-19

<150> US 60/108,379

<151> 1998-10-29

<150> US 09/150,857

<151> 1998-09-10

<160> 17

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1196

<212> DNA

<213> Mus musculus

<400> 1

agatgagtgt	ggggcgctcga	agagtcaagt	tgctgggcat	cctgatgatg	gcaaagtgtct	60
tcattttattt	gattgtggaa	gtctccaaaa	acagtagcca	agacaaaaat	ggaaagggag	120
gagtaataat	cccgaaagag	aagttctgga	agccaccag	cactccccgg	gcatactgga	180
acagggaaca	ggagaagctg	aacagggtgt	acaatcccat	cttgaacagg	gtggccaatc	240
agacagggga	gctagccaca	tctccaaaca	caagtcacct	gagctattgt	gaaccagact	300
cgacggtcac	gacagctgtg	acagatttta	ataatctgcc	ggacagattt	aaagactttc	360
tcttgtattt	gagatgccgg	aattactcgc	tgcttataga	tcaaccgaag	aaatgtgcaa	420
agaagccctt	cttactattg	gcgataaagt	ccctcattcc	acattttgcc	agaaggcaag	480
caattcggga	gtcttggggc	cgagaaacca	acgtaggga	ccagacagta	gtgagggctc	540
tcctgttgga	caagacaccc	ccagaggaca	accaccctga	cctttcggac	atgcttaagt	600
ttgagagtga	caagcaccag	gacatcctca	tgtggaacta	tagagacaca	ttcttcaacc	660
tgtccctgaa	ggaagtgtct	tttcttaggt	gggtgagcac	ttcctgtcca	gacgcagagt	720
ttgtcttcaa	gggcgatgat	gacgtgtttg	tgaacaccca	tcacatcctt	aattacttga	780
atagcttatc	caagagcaaa	gccaaagact	tggtcatagg	tgacgtgatc	cacaatgctg	840
ggcctcaccg	ggataagaaa	ctgaagtact	acatcccaga	agtcttctac	accggcgtct	900
acccaccgta	tgccgggggt	ggtggattcc	tgtactccgg	cccccttgcc	ttgaggctgt	960
acagtgcgac	tagccgggtc	catctctacc	ctattgatga	tggtttatacg	ggaatgtgcc	1020
ttcagaaaact	gggccttggt	ccagagaagc	acaaaggctt	caggacattt	gatattgaag	1080
agaaaaataa	gaaaaatatt	tgttcctata	tagacctaat	gtagtagcat	agcagaaaac	1140
ctcaagagat	gattgatatc	tggtctcagt	tgcaaagtcc	taatttaaaa	tgctga	1196

<210> 2

<211> 397

<212> PRT

<213> Mus musculus

<400> 2

Met	Ser	Val	Gly	Arg	Arg	Arg	Val	Lys	Leu	Leu	Gly	Ile	Leu	Met	Met
1				5				10					15		
Ala	Asn	Val	Phe	Ile	Tyr	Leu	Ile	Val	Glu	Val	Ser	Lys	Asn	Ser	Ser
			20					25					30		

Gln Asp Lys Asn Gly Lys Gly Gly Val Ile Ile Pro Lys Glu Lys Phe
 35 40 45
 Trp Lys Pro Pro Ser Thr Pro Arg Ala Tyr Trp Asn Arg Glu Gln Glu
 50 55 60
 Lys Leu Asn Arg Trp Tyr Asn Pro Ile Leu Asn Arg Val Ala Asn Gln
 65 70 75 80
 Thr Gly Glu Leu Ala Thr Ser Pro Asn Thr Ser His Leu Ser Tyr Cys
 85 90 95
 Glu Pro Asp Ser Thr Val Met Thr Ala Val Thr Asp Phe Asn Asn Leu
 100 105 110
 Pro Asp Arg Phe Lys Asp Phe Leu Tyr Leu Arg Cys Arg Asn Tyr
 115 120 125
 Ser Leu Leu Ile Asp Gln Pro Lys Lys Cys Ala Lys Lys Pro Phe Leu
 130 135 140
 Leu Leu Ala Ile Lys Ser Leu Ile Pro His Phe Ala Arg Arg Gln Ala
 145 150 155 160
 Ile Arg Glu Ser Trp Gly Arg Glu Thr Asn Val Gly Asn Gln Thr Val
 165 170 175
 Val Arg Val Phe Leu Leu Gly Lys Thr Pro Pro Glu Asp Asn His Pro
 180 185 190
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Asp Lys His Gln Asp Ile
 195 200 205
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
 210 215 220
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Ala Glu Phe
 225 230 235 240
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
 245 250 255
 Asn Tyr Leu Asn Ser Leu Ser Lys Ser Lys Ala Lys Asp Leu Phe Ile
 260 265 270
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
 275 280 285
 Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala
 290 295 300
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly Pro Ala Leu Leu Arg Leu Tyr
 305 310 315
 Ser Ala Thr Ser Arg Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
 325 330 335
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
 340 345 350
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser
 355 360 365
 Tyr Ile Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
 370 375 380
 Asp Ile Trp Ser Gln Leu Gln Ser Pro Asn Leu Lys Cys
 385 390 395

<210> 3
 <211> 1191
 <212> DNA
 <213> Mus musculus

<400> 3
 atgagtgttg ggcgtcgaag agtcaagttg ctgggcatcc tgatgatggc aaatgtcttc 60
 atttatttga ttgtggaagt ctccaaaaac agtagccaag acaaaaatgg aaagggaggga 120
 gtaataatcc cgaaagagaa gttctggaag ccaccagca ctccccgggc atactggaac 180
 agggaaacagg agaagctgaa caggtggtac aatcccctct tgaacagggt ggccaatcag 240
 acagggggagc tagccacatc tccaaacaca agtcacctga gctattgtga accagactcg 300
 acggtcattga cagctgtgac agattttaat aatctgccgg acagatttaa agactttctc 360
 ttgtatttga gatgccgga ttactcgtg cttatagatc aaccgaagaa atgtgcaaag 420
 aagcccttct tactattggc gataaagtcc ctcattccac attttgccag aaggcaagca 480
 attcgggagat cttgggggccc agaaaccaac gtagggaacc agacagtagt gaggggtcttc 540

```

ctgttgggca agacaccccc agaggacaac caccctgacc tttcggacat gcttaagttt 600
gagagtgaca agcaccagga catcctcatg tggaactata gagacacatt cttcaacctg 660
tccttgaagg aagtgtgtgt tcttaggtgg gtgagcactt cctgtccaga cgcagagttt 720
gtcttcaagg gcgatgatga cgtgtttgtg aacacccatc acatccttaa ttacttgaat 780
agcttatcca agagcaaagc caaagacttg ttcataagtg acgtgatcca caatgctggg 840
cctcaccggg ataagaaact gaagtactac atcccagaag tcttctacac cggcgtctac 900
ccaccgtatg ccgggggtgg tggattcctg tactccggcc cccttgctt gaggtgtac 960
agtgcgacta gccgggtcca tctctaccct attgatgatg tttatacggg aatgtgcctt 1020
cagaaactgg gccttgttcc agagaagcac aaaggcttca ggacatttga tattgaagag 1080
aaaaataaga aaaatatttg ttcctatata gacctaatgt tagtacatag cagaaaacct 1140
caagagatga ttgatatctg gtctcagttg caaagtccta atttaaaatg c 1191

```

```

<210> 4
<211> 365
<212> PRT
<213> Mus musculus

```

```

<400> 4
Gln Asp Lys Asn Gly Lys Gly Gly Val Ile Ile Pro Lys Glu Lys Phe
 1      5      10
Trp Lys Pro Pro Ser Thr Pro Arg Ala Tyr Trp Asn Arg Glu Gln Glu
      20      25      30
Lys Leu Asn Arg Trp Tyr Asn Pro Ile Leu Asn Arg Val Ala Asn Gln
      35      40      45
Thr Gly Glu Leu Ala Thr Ser Pro Asn Thr Ser His Leu Ser Tyr Cys
      50      55      60
Glu Pro Asp Ser Thr Val Met Thr Ala Val Thr Asp Phe Asn Asn Leu
      65      70      75      80
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
      85      90      95
Ser Leu Leu Ile Asp Gln Pro Lys Lys Cys Ala Lys Lys Pro Phe Leu
      100      105      110
Leu Leu Ala Ile Lys Ser Leu Ile Pro His Phe Ala Arg Arg Gln Ala
      115      120      125
Ile Arg Glu Ser Trp Gly Arg Glu Thr Asn Val Gly Asn Gln Thr Val
      130      135      140
Val Arg Val Phe Leu Leu Gly Lys Thr Pro Pro Glu Asp Asn His Pro
      145      150      155      160
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Asp Lys His Gln Asp Ile
      165      170      175
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
      180      185      190
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Ala Glu Phe
      195      200      205
Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
      210      215      220
Asn Tyr Leu Asn Ser Leu Ser Lys Ser Lys Ala Lys Asp Leu Phe Ile
      225      230      235      240
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
      245      250      255
Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala
      260      265      270
Gly Gly Gly Gly Phe Leu Tyr Ser Gly Pro Ala Leu Leu Arg Leu Tyr
      275      280      285
Ser Ala Thr Ser Arg Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
      290      295      300
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
      305      310      315      320
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser
      325      330      335
Tyr Ile Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
      340      345      350

```

Asp Ile Trp Ser Gln Leu Gln Ser Pro Asn Leu Lys Cys
 355 360 365

<210> 5
 <211> 1203
 <212> DNA
 <213> Mus musculus

<400> 5
 atgatttgcc cttcagcttt actggttatt ttaagaaatt taatacggga agaaaaaatc 60
 atttctcaag agatcctcaa tttgattgaa ttaaggatga aaaaaggga tattcagttg 120
 acaaaactctg caatcagtga tgcattaaaa gaaatcgata gtagtggtgt caatgttgct 180
 gtcaccgggg agacgggatc aggggaagtcc agcttcatca ataccctgag aggcattggg 240
 aatgaagaag aaggtgcagc taaaactggg gtggtggagg taaccatgga aagacatcca 300
 taaaaacacc ccaatatacc caatgtggtt ttttgggacc tgccctgggat tggaagcaca 360
 aatttccac caaacactta cctggagaaa atgaagttct atgagtacga tttcttcatt 420
 attatttcgg ccacacgctt caagaaaaat gatatagaca ttgccaaagc aatcagcatg 480
 atgaagaagg aattctactt cgtgagaacc aaggtggact ctgacataac aaatgaagca 540
 gatggcaaac ctcaaaccct tgacaaagaa aaggtcctgc aggacatccg ccttaactgt 600
 gtgaacacct ttagggagaa tggcattgct gagccaccaa tcttctgct ctctaacaaa 660
 aatgtttgtc actatgactt ccccgctctg atggacaagc tgataagtga cctccctatc 720
 tacaggagac acaattttat ggtctcctta cccaatatca cagattcagt cattgaaaag 780
 aagcggcaat ttctgaagca raggatttgg ctggaaggat ttgctgctga cctagtgaat 840
 atcatccctt ctctgacctt tctcttgac agtgatttgg agactctgaa gaaaagcatg 900
 aaattctacc gcactgtgtt tggagtggat gaaacatctt tgcagagatt agctagggac 960
 tgggaaatag aggtggatca ggtggaggcc atgataaaat ctctgctgt gttcaaacct 1020
 acagatgaag aaacaatata agaaaggctt tcaagatata ttcaggagtt ctgtttggct 1080
 aatgggtact tacttcctaa aaatagtttt cttaaagaaa tattttacct gaaatattat 1140
 ttccttgaca tgggtgactga ggatgctaaa actcttctta aagagatatg tttaagaaac 1200
 tag 1203

<210> 6
 <211> 400
 <212> PRT
 <213> Mus musculus

<400> 6
 Met Ile Cys Pro Ser Ala Leu Leu Val Ile Leu Arg Asn Leu Ile Arg
 1 5 10 15
 Glu Glu Lys Ile Ile Ser Gln Glu Ile Leu Asn Leu Ile Glu Leu Arg
 20 25 30
 Met Lys Lys Gly Asn Ile Gln Leu Thr Asn Ser Ala Ile Ser Asp Ala
 35 40 45
 Leu Lys Glu Ile Asp Ser Ser Val Leu Asn Val Ala Val Thr Gly Glu
 50 55 60
 Thr Gly Ser Gly Lys Ser Phe Ile Asn Thr Leu Arg Gly Ile Gly
 65 70 75 80
 Asn Glu Glu Glu Gly Ala Ala Lys Thr Gly Val Val Glu Val Thr Met
 85 90 95
 Glu Arg His Pro Tyr Lys His Pro Asn Ile Pro Asn Val Val Phe Trp
 100 105 110
 Asp Leu Pro Gly Ile Gly Ser Thr Asn Phe Pro Pro Asn Thr Tyr Leu
 115 120 125
 Glu Lys Met Lys Phe Tyr Glu Tyr Asp Phe Phe Ile Ile Ile Ser Ala
 130 135 140
 Thr Arg Phe Lys Lys Asn Asp Ile Asp Ile Ala Lys Ala Ile Ser Met
 145 150 155 160
 Met Lys Lys Glu Phe Tyr Phe Val Arg Thr Lys Val Asp Ser Asp Ile
 165 170 175
 Thr Asn Glu Ala Asp Gly Lys Pro Gln Thr Phe Asp Lys Glu Lys Val
 180 185 190

Leu Gln Asp Ile Arg Leu Asn Cys Val Asn Thr Phe Arg Glu Asn Gly
 195 200 205
 Ile Ala Glu Pro Pro Ile Phe Leu Leu Ser Asn Lys Asn Val Cys His
 210 215 220
 Tyr Asp Phe Pro Val Leu Met Asp Lys Leu Ile Ser Asp Leu Pro Ile
 225 230 235 240
 Tyr Arg Arg His Asn Phe Met Val Ser Leu Pro Asn Ile Thr Asp Ser
 245 250 255
 Val Ile Glu Lys Lys Arg Gln Phe Leu Lys Gln Arg Ile Trp Leu Glu
 260 265 270
 Gly Phe Ala Ala Asp Leu Val Asn Ile Ile Pro Ser Leu Thr Phe Leu
 275 280 285
 Leu Asp Ser Asp Leu Glu Thr Leu Lys Lys Ser Met Lys Phe Tyr Arg
 290 295 300
 Thr Val Phe Gly Val Asp Glu Thr Ser Leu Gln Arg Leu Ala Arg Asp
 305 310 315 320
 Trp Glu Ile Glu Val Asp Gln Val Glu Ala Met Ile Lys Ser Pro Ala
 325 330 335
 Val Phe Lys Pro Thr Asp Glu Glu Thr Ile Gln Glu Arg Leu Ser Arg
 340 345 350
 Tyr Ile Gln Glu Phe Cys Leu Ala Asn Gly Tyr Leu Leu Pro Lys Asn
 355 360 365
 Ser Phe Leu Lys Glu Ile Phe Tyr Leu Lys Tyr Tyr Phe Leu Asp Met
 370 375 380
 Val Thr Glu Asp Ala Lys Thr Leu Leu Lys Glu Ile Cys Leu Arg Asn
 385 390 395 400

<210> 7
 <211> 1200
 <212> DNA
 <213> Mus musculus

<400> 7
 atgatttgcc cttcagcttt actggttatt ttaagaaatt taatacggga agaaaaaatc 60
 atttctcaag agatcctcaa tttgattgaa ttaaggatga aaaaaggga tattcagttg 120
 acaaactctg caatcagtga tgcattaaaa gaaatcgata gtagtgtgct caatggtgct 180
 gtcaccgggg agacgggatc agggaagtcc agcttcatca ataccctgag aggcatggg 240
 aatgaagaag aagggtgcagc taaaactggg gtggtggagg taaccatgga aagacatcca 300
 taaaaacacc ccaatatacc caatgtggtt ttttgggacc tgcctgggat tgggaagcaca 360
 aatttccac caaacactta cctggagaaa atgaagtct atgagtacga tttcttcatt 420
 attatttcgg ccacacgctt caagaaaaat gatatagaca ttgccaaagc aatcagcatg 480
 atgaagaagg aattctactt cgtgagaacc aagggtggact ctgacataac aatgaagca 540
 gatggcaaac ctcaaacctt tgacaaagaa aaggtcctgc aggacatccg ccttaactgt 600
 gtgaacacct ttaggagaaa tggcattgct gagccaccaa tcttcctgct ctctaacaaa 660
 aatgtttgtc actatgactt ccccgctcctg atggacaagc tgataagtga cctccctatc 720
 tacaggagac acaattttat ggtctcctta cccaatatca cagattcagt cattgaaaag 780
 aagcggcaat ttctgaagca raggatttgg ctggaaggat ttgctgctga cctagtgaat 840
 atcatccctt ctctgacctt tctcttgac agtgatttgg agactctgaa gaaaagcatg 900
 aaattctacc gcactgtggt tggagtggat gaaacatctt tgcagagatt agctagggac 960
 tgggaaatag aggtggatca ggtggaggcc atgataaaat ctcctgctgt gttcaaacct 1020
 acagatgaag aaacaatata agaaaggctt tcaagatata ttcaggagtt ctggttggct 1080
 aatgggtact tacttcctaa aaatagtttt cttaaagaaa tattttacct gaaatattat 1140
 ttccttgaca tgggtgactga ggatgctaaa actcttctta aagagatatg tttaagaaac 1200

<210> 8
 <211> 326
 <212> PRT
 <213> Mus musculus

<400> 8
 Met Ala Ser Lys Val Ser Cys Leu Tyr Val Leu Ser Val Val Cys Trp
 1 5 10 15

Ala Ser Ala Leu Trp Tyr Leu Ser Ile Thr Arg Pro Thr Ser Ser Tyr
 20 25 30
 Thr Gly Ser Lys Pro Phe Ser His Leu Thr Val Ala Arg Lys Asn Phe
 35 40 45
 Thr Phe Gly Asn Ile Arg Thr Arg Pro Ile Asn Pro His Ser Phe Glu
 50 55 60
 Phe Leu Ile Asn Glu Pro Asn Lys Cys Glu Lys Asn Ile Pro Phe Leu
 65 70 75 80
 Val Ile Leu Ile Ser Thr Thr His Lys Glu Phe Asp Ala Arg Gln Ala
 85 90 95
 Ile Arg Glu Thr Trp Gly Asp Glu Asn Asn Phe Lys Gly Ile Lys Ile
 100 105 110
 Ala Thr Leu Phe Leu Leu Gly Lys Asn Ala Asp Pro Val Leu Asn Gln
 115 120 125
 Met Val Glu Gln Glu Ser Gln Ile Phe His Asp Ile Ile Val Glu Asp
 130 135 140
 Phe Ile Asp Ser Tyr His Asn Leu Thr Leu Lys Thr Leu Met Gly Met
 145 150 155 160
 Arg Trp Val Ala Thr Phe Cys Ser Lys Ala Lys Tyr Val Met Lys Thr
 165 170 175
 Asp Ser Asp Ile Phe Val Asn Met Asp Asn Leu Ile Tyr Lys Leu Leu
 180 185 190
 Lys Pro Ser Thr Lys Pro Arg Arg Tyr Phe Thr Gly Tyr Val Ile
 195 200 205
 Asn Gly Gly Pro Ile Arg Asp Val Arg Ser Lys Trp Tyr Met Pro Arg
 210 215 220
 Asp Leu Tyr Pro Asp Ser Asn Tyr Pro Pro Phe Cys Ser Gly Thr Gly
 225 230 235 240
 Tyr Ile Phe Ser Ala Asp Val Ala Glu Leu Ile Tyr Lys Thr Ser Leu
 245 250 255
 His Thr Arg Leu Leu His Leu Glu Asp Val Tyr Val Gly Leu Cys Leu
 260 265 270
 Arg Lys Leu Gly Ile His Pro Phe Gln Asn Ser Gly Phe Asn His Trp
 275 280 285
 Lys Met Ala Tyr Ser Leu Cys Arg Tyr Arg Arg Val Ile Thr Val His
 290 295 300
 Gln Ile Ser Pro Glu Glu Met His Arg Ile Trp Asn Asp Met Ser Ser
 305 310 315 320
 Lys Lys His Leu Arg Cys
 325

<210> 9
 <211> 331
 <212> PRT
 <213> Mus musculus

<400> 9
 Met Ala Pro Ala Val Leu Thr Ala Leu Pro Asn Arg Met Ser Leu Arg
 1 5 10 15
 Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe Leu Val
 20 25 30
 Ile Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu Arg Val Asn
 35 40 45
 Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg Gln Asp Phe Arg
 50 55 60
 Phe Thr Leu Arg Glu His Ser Asn Cys Ser His Gln Asn Pro Phe Leu
 65 70 75 80
 Val Ile Leu Val Thr Ser Arg Pro Ser Asp Val Lys Ala Arg Gln Ala
 85 90 95
 Ile Arg Val Thr Trp Gly Glu Lys Lys Ser Trp Trp Gly Tyr Glu Val
 100 105 110

Leu Thr Phe Phe Leu Leu Gly Gln Gln Ala Glu Arg Glu Asp Lys Thr
 115 120 125
 Leu Ala Leu Ser Leu Glu Asp Glu His Val Leu Tyr Gly Asp Ile Ile
 130 135 140
 Arg Gln Asp Phe Leu Asp Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile
 145 150 155 160
 Met Ala Phe Arg Trp Val Met Glu Phe Cys Pro Asn Ala Lys Tyr Ile
 165 170 175
 Met Lys Thr Asp Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys
 180 185 190
 Tyr Leu Leu Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro
 195 200 205
 Leu Ile Asp Asn Tyr Ser Tyr Arg Gly Phe Phe His Lys Asn His Ile
 210 215 220
 Ser Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly
 225 230 235 240
 Leu Gly Tyr Ile Met Ser Gly Asp Leu Val Pro Arg Val Tyr Glu Met
 245 250 255
 Met Ser His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val Gly Ile
 260 265 270
 Cys Leu Asn Leu Leu Lys Val Asp Ile His Ile Pro Glu Asp Thr Asn
 275 280 285
 Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys Gln Leu Arg Arg
 290 295 300
 Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu Ile Thr Phe Trp
 305 310 315 320
 Gln Val Met Leu Arg Asn Thr Thr Cys His Tyr
 325 330

<210> 10

<211> 325

<212> PRT

<213> Drosophilea melonogaster

<400> 10

Met Gln Ser Lys His Arg Lys Leu Leu Leu Arg Cys Leu Leu Val Leu
 1 5 10 15
 Pro Leu Ile Leu Leu Val Asp Tyr Cys Gly Leu Leu Thr His Leu His
 20 25 30
 Glu Leu Asn Phe Glu Arg His Phe His Tyr Pro Leu Asn Asp Asp Thr
 35 40 45
 Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg
 50 55 60
 Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu
 65 70 75 80
 Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala
 85 90 95
 Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu
 100 105 110
 Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val
 115 120 125
 Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr
 130 135 140
 Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp
 145 150 155 160
 Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp
 165 170 175
 Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly
 180 185 190
 Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln
 195 200 205

Thr	Ser	Pro	Leu	Arg	His	Lys	Phe	Ser	Lys	Trp	Tyr	Val	Ser	Leu	Glu
	210					215					220				
Glu	Tyr	Pro	Phe	Asp	Arg	Trp	Pro	Pro	Tyr	Val	Thr	Ala	Gly	Ala	Phe
225					230					235					240
Ile	Leu	Ser	Gln	Lys	Ala	Leu	Arg	Gln	Leu	Tyr	Ala	Ala	Ser	Val	His
				245						250				255	
Leu	Pro	Leu	Phe	Arg	Phe	Asp	Asp	Val	Tyr	Leu	Gly	Ile	Val	Ala	Leu
			260					265					270		
Lys	Ala	Gly	Ile	Ser	Leu	Gln	His	Cys	Asp	Asp	Phe	Arg	Phe	His	Arg
		275					280					285			
Pro	Ala	Tyr	Lys	Gly	Pro	Asp	Ser	Tyr	Ser	Ser	Val	Ile	Ala	Ser	His
	290					295					300				
Glu	Phe	Gly	Asp	Pro	Glu	Glu	Met	Thr	Arg	Val	Trp	Asn	Glu	Cys	Arg
305					310					315					320
Ser	Ala	Asn	Tyr	Ala											
				325											

<210> 11
 <211> 422
 <212> PRT
 <213> Homo sapien

<400> 11

Met	Leu	Gln	Trp	Arg	Arg	Arg	His	Cys	Cys	Phe	Ala	Lys	Met	Thr	Trp
1				5					10					15	
Asn	Ala	Lys	Arg	Ser	Leu	Phe	Arg	Thr	His	Leu	Ile	Gly	Val	Leu	Ser
			20					25					30		
Leu	Val	Phe	Leu	Phe	Ala	Met	Phe	Leu	Phe	Phe	Asn	His	His	Asp	Trp
		35					40					45			
Leu	Pro	Gly	Arg	Ala	Gly	Phe	Lys	Glu	Asn	Pro	Val	Thr	Tyr	Thr	Phe
	50					55				60					
Arg	Gly	Phe	Arg	Ser	Thr	Lys	Ser	Glu	Thr	Asn	His	Ser	Ser	Leu	Arg
65					70					75					80
Asn	Ile	Trp	Lys	Glu	Thr	Val	Pro	Gln	Thr	Leu	Arg	Pro	Gln	Thr	Ala
			85					90						95	
Thr	Asn	Ser	Asn	Asn	Thr	Asp	Leu	Ser	Pro	Gln	Gly	Val	Thr	Gly	Leu
			100				105						110		
Glu	Asn	Thr	Leu	Ser	Ala	Asn	Gly	Ser	Ile	Tyr	Asn	Glu	Lys	Gly	Thr
		115					120					125			
Gly	His	Pro	Asn	Ser	Tyr	His	Phe	Lys	Tyr	Ile	Ile	Asn	Glu	Pro	Glu
	130					135					140				
Lys	Cys	Gln	Glu	Lys	Ser	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Ala	Glu
145					150					155					160
Pro	Gly	Gln	Ile	Glu	Ala	Arg	Arg	Ala	Ile	Arg	Gln	Thr	Trp	Gly	Asn
				165					170					175	
Glu	Ser	Leu	Ala	Pro	Gly	Ile	Gln	Ile	Thr	Arg	Ile	Phe	Leu	Leu	Gly
			180					185					190		
Leu	Ser	Ile	Lys	Leu	Asn	Gly	Tyr	Leu	Gln	Arg	Ala	Ile	Leu	Glu	Glu
		195					200					205			
Ser	Arg	Gln	Tyr	His	Asp	Ile	Ile	Gln	Gln	Glu	Tyr	Leu	Asp	Thr	Tyr
	210					215					220				
Tyr	Asn	Leu	Thr	Ile	Lys	Thr	Leu	Met	Gly	Met	Asn	Trp	Val	Ala	Thr
225					230					235					240
Tyr	Cys	Pro	His	Ile	Pro	Tyr	Val	Met	Lys	Thr	Asp	Ser	Asp	Met	Phe
				245					250					255	
Val	Asn	Thr	Glu	Tyr	Leu	Ile	Asn	Lys	Leu	Leu	Lys	Pro	Asp	Leu	Pro
			260					265					270		
Pro	Arg	His	Asn	Tyr	Phe	Thr	Gly	Tyr	Leu	Met	Arg	Gly	Tyr	Ala	Pro
		275					280					285			
Asn	Arg	Asn	Lys	Asp	Ser	Lys	Trp	Tyr	Met	Pro	Pro	Asp	Leu	Tyr	Pro
	290					295					300				

Ser Glu Arg Tyr Pro Val Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser
 305 310 315 320
 Gly Asp Leu Ala Glu Lys Ile Phe Lys Val Ser Leu Gly Ile Arg Arg
 325 330 335
 Leu His Leu Glu Asp Val Tyr Val Gly Ile Cys Leu Ala Lys Leu Arg
 340 345 350
 Ile Asp Pro Val Pro Pro Pro Asn Glu Phe Val Phe Asn His Trp Arg
 355 360 365
 Val Ser Tyr Ser Ser Cys Lys Tyr Ser His Leu Ile Thr Ser His Gln
 370 375 380
 Phe Gln Pro Ser Glu Leu Ile Lys Tyr Trp Asn His Leu Gln Gln Asn
 385 390 395 400
 Lys His Asn Ala Cys Ala Asn Ala Ala Lys Glu Lys Ala Gly Arg Tyr
 405 410 415
 Arg His Arg Lys Leu His
 420

<210> 12
 <211> 229
 <212> PRT
 <213> Artificial sequence

<220>
 <221> VARIANT
 <222> (1)...(229)
 <223> Xaa = Any Amino Acid

<400> 12
 Met Ala Xaa Arg Arg Lys Val Leu Leu Arg Leu Leu Val Leu Ser Leu
 1 5 10 15
 Val Xaa Leu Xaa Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Phe Pro
 20 25 30
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser
 35 40 45
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn
 50 55 60
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe
 65 70 75 80
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu
 85 90 95
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala
 100 105 110
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val
 115 120 125
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa
 130 135 140
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile
 145 150 155 160
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu
 165 170 175
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val
 180 185 190
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn
 195 200 205
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly
 210 215 220
 Tyr Val Ile Xaa Gly
 225

<210> 13
 <211> 1707
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (246)...(1436)

<221> misc_feature

<222> (1)...(1707)

<223> n = A,T,C or G

<400> 13

acgcgtccgc gcagcggcag cggcagcagc ggcaacaagt gccggaggct agcagagcca	60
agccggagca gtccctgccg ccgacaccgc cgggccgccc gtccggggcg ccgcgcattg	120
agcgtgagct gcggcggtcg ccgggctgag ccgcgcggag cggccgggac gtggatgtgg	180
ccgcgatctc ccgcccttgc ccccgccccg ccgagctgga gctgctcccg gacaagatat	240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg	290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met	
1 5 10 15	
atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt	338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser	
20 25 30	
agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag	386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys	
35 40 45	
ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa	434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln	
50 55 60	
gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac	482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn	
65 70 75	
cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac	530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr	
80 85 90 95	
tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac	578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn	
100 105 110	
ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat	626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn	
115 120 125	
tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc	674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe	
130 135 140	
ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa	722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln	
145 150 155	
gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg	770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr	
160 165 170 175	
gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac	818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His	
180 185 190	

ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac 866
 Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp
 195 200 205
 att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag 914
 Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys
 210 215 220
 gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag 962
 Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu
 225 230 235
 ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc 1010
 Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile
 240 245 250 255
 ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc 1058
 Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe
 260 265 270
 ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg 1106
 Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu
 275 280 285
 aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat 1154
 Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr
 290 295 300
 gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg 1202
 Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu
 305 310 315
 tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat 1250
 Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr
 320 325 330 335
 act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa 1298
 Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys
 340 345 350
 ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc 1346
 Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys
 355 360 365
 tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg 1394
 Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met
 370 375 380
 att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc 1436
 Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 385 390 395
 taaaatagat acaaaactcaa tttkgsatwg raagggggtwt tttgratwgg ycccatgttg 1496
 ggggtctcaca ttagagtaat ttctatttna ancatgaaat tgcctttatg agtgataccc 1556
 atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta 1616
 atttntttat ggtgaatggc aggatattgg tctgacttac cgntagggga ntttaaaact 1676
 ggnoccttttt gaatctgttt ggatggccct t 1707

<210> 14

<211> 397

<212> PRT
<213> Homo sapiens

<400> 14
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met
1 5 10 15
Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser
20 25 30
Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
35 40 45
Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
50 55 60
Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
65 70 75 80
Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
85 90 95
Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
100 105 110
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
115 120 125
Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
130 135 140
Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala
145 150 155 160
Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
165 170 175
Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
180 185 190
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
195 200 205
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
210 215 220
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
225 230 235 240
Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
245 250 255
Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
260 265 270
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
275 280 285
Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
290 295 300
Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
305 310 315 320
His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
325 330 335
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
340 345 350
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
355 360 365
Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
370 375 380
Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
385 390 395

<210> 15
<211> 365
<212> PRT
<213> Homo sapiens

<400> 15
 Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
 1 5 10 15
 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
 20 25 30
 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
 35 40 45
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
 50 55 60
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
 65 70 75 80
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
 85 90 95
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
 100 105 110
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Gln Ala
 115 120 125
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
 130 135 140
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
 145 150 155 160
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
 165 170 175
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
 180 185 190
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
 195 200 205
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
 210 215 220
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
 225 230 235 240
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
 245 250 255
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
 260 265 270
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
 275 280 285
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
 290 295 300
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
 305 310 315 320
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
 325 330 335
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
 340 345 350
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 355 360 365

<210> 16

<211> 20

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> (1)...(20)

<223> Synthetically generated primer

<400> 16

cttcgacgcc ccacactcat

<210> 17
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> (1)...(20)
<223> Synthetically generated primer

<400> 17
atgagtgtgg ggcgtcgaag